

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2003, 15:26:12 ; Search time 94 Seconds
(without alignments)
2591.952 Million cell updates/sec.

Title: US-09-868-987-14

Perfect score: 2778

Sequence: 1 MVSSPILNVPLKXHASVSGK.....SLYIAPPLLLPMVRKRNRSK 552

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0		Ygapext 0.5	
Ygapop 6.0		Ygapext 7.0	
Delop 6.0		Delext 7.0	

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09868987/runat 28102003 152602 23852/app query.fasta_1.711
-DB=Issued Patents NA -QWMT=fastcap -SUFFIX=rni -MINWATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09868987 @CGN 1 1 56 @runat 28102003 152602 23852 -NCPU=6 -ICPU=3
-NO MMAP -LARGJQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	2730	98.3	1230025	4	US-09-198-452A-1
C 2	719	25.9	1830121	4	US-09-557-884-1
C 3	719	25.9	1830121	4	US-09-643-990A-1
C 4	678.5	24.4	2211	3	US-09-462-844-1
C 5	672	24.2	6321	4	US-09-221-017B-311
C 6	646.5	23.3	2301	4	US-09-134-001C-852
C 7	512	18.4	4403765	3	US-09-103-840A-2
C 8	509	18.3	4411529	3	US-09-103-840A-1
C 9	483.5	17.4	40429	4	US-08-311-731A-125
C 10	425	15.3	1398	4	US-09-252-991A-6413
C 11	418	15.0	1947	4	US-09-328-352-1027
C 12	417	15.0	1890	4	US-09-252-991A-6330

13 369.5 13.3 969 4 US-09-252-991A-6245 Sequence 6245, Ap
C 14 369.5 13.3 984 4 US-09-252-991A-6054 Sequence 6054, Ap
C 15 358 12.9 429 4 US-09-252-991A-6217 Sequence 6217, Ap
C 16 314 11.3 870 4 US-09-252-991A-6138 Sequence 6138, Ap
C 17 306.5 11.0 996 4 US-09-328-352-1243 Sequence 1243, Ap
C 18 170.5 6.1 1664976 4 US-08-916-421B-1 Sequence 1, Appli
19 138 5.0 3102 4 US-09-252-991A-4040 Sequence 4040, Ap
20 138 5.0 4284 4 US-09-252-991A-4006 Sequence 4006, Ap
C 21 138 5.0 4704 4 US-09-252-991A-3906 Sequence 3906, Ap
22 137.5 4.9 3120 4 US-09-328-352-1348 Sequence 1348, Ap
23 136 4.9 3096 5 PCT-US96-05320A-897 Sequence 897, App
24 136 4.9 3156 4 US-09-134-001C-2168 Sequence 2168, Ap
25 136 4.9 1830121 4 US-09-557-884-1 Sequence 1, Appli
26 136 4.9 1830121 4 US-09-643-990A-1 Sequence 1, Appli
27 132 4.8 1664976 4 US-08-916-421B-1 Sequence 1, Appli
C 28 128.5 4.6 3201 4 US-09-252-991A-14959 Sequence 14959, A
29 128.5 4.6 3402 4 US-09-252-991A-14791 Sequence 14791, A
C 30 127 4.6 288 4 US-09-134-001C-829 Sequence 829, App
C 31 126.5 4.6 15393 4 US-09-453-702B-191 Sequence 191, App
32 124 4.5 3003 4 US-09-252-991A-14790 Sequence 14790, A
33 124 4.5 3132 4 US-09-252-991A-14540 Sequence 14540, A
C 34 124 4.5 3411 4 US-09-252-991A-14823 Sequence 14823, A
C 35 123.5 4.4 2862 4 US-09-252-991A-443 Sequence 443, App
36 123.5 4.4 3102 4 US-09-328-352-1012 Sequence 1012, App
37 123.5 4.4 3156 4 US-09-252-991A-418 Sequence 418, App
C 38 123 4.4 2862 4 US-09-252-991A-10659 Sequence 10659, A
39 123 4.4 2910 4 US-09-252-991A-10414 Sequence 10414, A
C 40 123 4.4 3111 4 US-09-252-991A-10504 Sequence 10504, A
41 122.5 4.4 1713 4 US-09-252-991A-14948 Sequence 14948, A
C 42 122.5 4.4 3144 4 US-09-252-991A-14688 Sequence 14688, A
43 122.5 4.4 3198 4 US-09-252-991A-15066 Sequence 15066, A
44 121.5 4.4 3186 4 US-09-328-352-319 Sequence 319, App
C 45 118.5 4.3 7886 4 US-09-453-702B-102 Sequence 102, App

ALIGNMENTS

RESULT 1

US-09-198-452A-1/c
Sequence 1, Application US/09198452A
Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (1) .. (15000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature

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OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature

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OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature

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OTHER INFORMATION: n=a or c or g or t

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OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature

LOCATION: (75001) .. (90000)

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[illegible]

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Alignment Scores:
 Pred. No.: 0 Length: 1230025
 Score: 2730.00 Matches: 551
 Percent Similarity: 99.28% Conservative: 0
 Best Local Similarity: 99.28% Mismatches: 1
 Query Match: 99.27% Indels: 3
 DB: 4 Gaps: 0

US-09-868-987-14 (1-552) x US-09-198-452A-1 (1-1230025)

QY 1 MetValSerSerProfilLeuAsnValProLeuLysAsnHisAlaSerValSerGlyLys 20
 Db 661906 ATGGTCAGCAGCCCTATTTAAACGTCCTCAATGAAATCATGCCAGTGTCTCAGGGAA 661847
 QY 21 PheThrHisArgGluValSerLysLeuAlaSerLeuLysSerGlyAlaMetSerPhe 40
 Db 661846 TTTACCCACCGTGAAGTCAGCAAACTCGCCCTCAGATTAAATCTGGAGCGATGCTTTT 661787
 QY 41 ValProGluValLeuSerGluGluThrIleSerSerPheLeuGlyLysGlnCysThr 60
 Db 661786 GTTCCCGAGGTTCTCAGTGAAGACGATCTCTCTGATCTTGGAAGAAACAAATGACA 661727
 QY 61 GlnGlyIlelleSerAlaCysGlyLeuAlaMetLeuIleValLeuMetSerValTyr 80
 Db 661726 CAAGCATTATCTCAGCATGCTGGCTTGGCAATGCTTATTTGATGAGCGTATAT 661667
 QY 81 TyrArgPheGlyGlyValIleAlaSerGlyAlaValLeuLeuLeuLeuLeuLeuLeu 100
 Db 661666 TATAGATTGGAGCGCTCATCGCTTCGGAGCTGCTTCTTGAATCTTTTGTCTATCTGG 661607
 QY 101 AlaAlaLeuGlnTyrLeuAspAlaProLeuThrLeuSerGlyLeuAlaGlyIleValLeu 120
 Db 661606 GCAGCTCTACAGATTGTTGGATGGCCACTCACCTTGTTCAGACTCGCTGGATTGTCCT 661547
 QY 121 AlaMetGlyMetAlaValAspAlaAsnValLeuValPheGluArgIleArgGluPhe 140
 Db 661546 GCTATGGGATGCCGCTAGATGCAATGTTCTGTATTTCGAAAGATCCGAGAGGAATTT 661487
 QY 141 LeuLeuSerGlnSerLeuLysSerValGlyLysGlyTyrThrLysAlaPheGlyAla 160
 Db 661486 TTATGTCTCAAGTCTTAAANAATCTGTAGAAAAAGGATATACCAAGGCTTTTGGAGCC 661427
 QY 161 IlePheAspSerAsnLeuThrValLeuAlaSerAlaLeuLeuPhePheLeuAspThr 180
 Db 661426 ATTTTGAATCTTAATGACTACAGATTGGCCCTCAGCACTCTTTTCTTCCTAGATACA 661367
 QY 181 GlyProIleLysGlyPheAlaLeuThrLeuLeuGlyIlePheSerSerMetPheThr 200
 Db 661366 GGGCCCTATTAAAGGGTTGCTTTGACATTGATTTAGGAATTTTCTCTTCAATGTTTACG 661307
 QY 201 AlaLeuPheMetThrLysPhePheMetLeuTyrMetAsnLysThrGlnHisThrGln 220

Db 661306 GCTCTTTTCATGACTAAATTTTCTTCATGCTGTGTGATGAATAAGACCAACATACACAG 661247
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 QY 241 LeuTrpAlaValSerGlySerValPheLeuLeuGlyCysValAlaLeuGlyPheGlyAla 260
 Db 661186 CTTTGGGCTGTTCTTGGAAAGTGTTTTCTTTAGTTCGGTTGCTCTCGGGTTTGGAGCC 661127
 QY 261 TrpAsnSerValLeuGlyMetAspPheLysGlyTyrAlaPheThrPheAsnProLys 280
 Db 661126 TGGAAATCCGTTTGGGAATGGAATTTAAAGAGGGATGTCCTTTACCTTTAATCCAAA 661067
 QY 281 GluHisGlyIleSerAspValAlaGlnMetArgGlyLysValValHisLysLeuGlnGlu 300
 Db 661066 GAGCATGGCATCAGCGATGTTGCTCAATCGTGGCAAGTTGTGCATAAATCAGGAA 661007
 QY 301 AlaGlyLeuSerSerArgAspPheArgIleGlnThrPheGlySerSerGlyLysLys 320
 Db 661006 GCTGGTCTTTCTCTAGAGACTTCGGTATTCAAAACATTTGCATCTTCAGAAAAAGATCAA 660947
 QY 321 IleTyrPheSerAspLysAlaLeuSerTyrThr-LysGlnIleArgAlaSerLeuLeuLys 340
 Db 660946 ATCTATTTTAGTGTATAAGCTTTAAGCTATACATAAGCAGATACGAGCCTCTCTCTAAA 660887
 QY 340 sLeuThrIleMetSerTrpArg-TyrCysGlyIleValValArgAsnArgProArgPheL 360
 Db 660886 ATTAACGATCATGAGCTGGCGTTAGCTGTGGGATTGTTGTTCAGNAACAGCCCTAGATTTC 660827
 QY 360 euTyrGlyAnSerLysArgAsnAlaLys-PheTrpSerLysValSerLysLeuSer 379
 Db 660826 TCTACGGAACTCTAAACGAAAGCAAAATTTTGGTCAAAAGGTAAACAGCAAACTATCG 660767
 QY 380 LysLysMetArgTyrGlnAlaThrIleGlyLeuLeuGlyAlaLeuAlaIleLeuLeu 399
 Db 660766 AAGAAATGCGTTATCAGGGCAGCATCGGCTTTTAGGAGCTTTGGCAATCATCTTCTC 660707
 QY 400 TyrValSerLeuArgPheGluTyrGlnTyrAlaPheSerAlaValCysAlaLeuIleHis 419
 Db 660706 TATGTGAGTTTGGCTTTGAAATGGCAATATGCTTTTCAGTGGCGTATCGCGTTTAAATTCAT 660647
 QY 420 AspLeuLeuAlaThrCysAlaValLeuPheIleAlaHisPhePheLeuLysLysIleGln 439
 Db 660646 GACCTTTGGCTACCTGTGCGAGTCTTGTATTATAGCACATTTCTTTTGAAGAAATTCAA 660587
 QY 440 IleAspLeuGlnAlaIleGlyAlaLeuMetThrValLeuGlyTyrSerLeuAsnAsnThr 459
 Db 660586 ATAGATTTCGAAGCCATTTGCTTTTAAAGCTGTTATGGGGTATTCTTAAACAAATACT 660527
 QY 460 LeuIlePheAspArgIleArgGluAspArgGlnAlaAsnLeuPheThrProMetHis 479
 Db 660526 TTGATCATTTTGTGCTATTCTGTAAGATCGCCAGCAACCTGTTTACCCCTATGCAT 660467
 QY 480 ValLeuValAsnAspAlaLeuGlnLysThrPheSerArgThrValMetThrThrAlaThr 499
 Db 660466 GTTTTAGTTAATGATGCCCTTCAAAAGACGTTTCAGCCGACGGTAATGACACAGCTACA 660407
 QY 500 ThrLeuSerValLeuLeuMetLeuLeuPheIleGlyGlySerValPheAsnPheAla 519
 Db 660406 ACTCTATCAGTTTGTAAATGCTTTTGTATTAGCGGCTCTCTGTCTTTAATTTTGA 660347
 QY 520 PheIleMetThrIleGlyIleLeuLeuGlyThrLeuSerSerLeuTyrIleAlaProPro 539
 Db 660346 TTTATTATGACCATAGGATCTCTTAGAACTTTTATCGTCTCTTTATATGCACCACT 660287
 QY 540 LeuLeuLeuPheMetValArgLysGlnAsnArgSerLys-552
 Db 660286 CTGTGTTGTTTATGGTCCGTAAGAAATCGCTCAAAA 660248

RESULT 2

US-09-557-884-1/c

; Sequence 1, Application US/09557884

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